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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:34:34 ; Search time 23.63 Seconds  
(without alignments)  
310.227 Million cell updates/sec

Title: US-09-653-755A-5

Perfect score: 1121  
Sequence: 1 ENVLTQSPRIMASPGKVT.....EATHTKTSPIYKSFNRNC 214

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	50.1	106	1 KAC_MOUSE	P01837 mus musculu
2	484	43.2	106	1 KACA_RAT	P01836 rattus norv
3	469	41.8	106	1 KACB_RAT	P01835 rattus norv
4	461.5	41.2	129	1 KVA4_MOUSE	P01680 mus musculu
5	430.5	38.4	107	1 KV6F_MOUSE	P04940 mus musculu
6	425.5	38.0	107	1 KV6I_MOUSE	P04943 mus musculu
7	424.5	37.9	107	1 KV6H_MOUSE	P04942 mus musculu
8	421.5	37.6	107	1 KV6G_MOUSE	P04941 mus musculu
9	420.5	37.5	107	1 KV6J_MOUSE	P01679 mus musculu
10	411.5	36.7	107	1 KV6A_MOUSE	P01675 mus musculu
11	411.5	36.7	107	1 KV6D_MOUSE	P01678 mus musculu
12	407.5	36.4	108	1 KV6K_MOUSE	P04945 mus musculu
13	405.5	36.2	107	1 KV6B_MOUSE	P01676 mus musculu
14	403.5	36.0	107	1 KV6C_MOUSE	P01677 mus musculu
15	396.5	35.4	107	1 KV6E_MOUSE	P01679 mus musculu
16	363.5	32.4	129	1 KV3L_HUMAN	P18135 homo sapien
17	360.5	32.2	109	1 KV3E_HUMAN	P01623 homo sapien
18	360.5	32.2	109	1 KV3F_HUMAN	P01624 homo sapien
19	353	31.5	106	1 KAC3_HUMAN	P01834 homo sapien
20	352.5	31.4	109	1 KV3B_HUMAN	P01620 homo sapien
21	352.5	31.4	129	1 KV3M_HUMAN	P18136 homo sapien
22	351	31.3	111	1 KV3R_MOUSE	P01670 mus musculu
23	349.5	31.2	109	1 KV3D_HUMAN	P01622 homo sapien
24	345	30.8	111	1 KV3J_MOUSE	P01662 mus musculu
25	344	30.7	129	1 KV1W_HUMAN	P04431 homo sapien
26	344	30.7	131	1 KV3I_MOUSE	P01661 mus musculu
27	343.5	30.6	107	1 KV1D_HUMAN	P01556 homo sapien
28	342	30.5	111	1 KV3H_MOUSE	P01660 mus musculu
29	340	30.3	111	1 KV3T_MOUSE	P01672 mus musculu
30	339.5	30.3	129	1 KV3H_HUMAN	P04207 homo sapien
31	338	30.2	108	1 KV5M_MOUSE	P01646 mus musculu
32	337	30.1	108	1 KV5O_MOUSE	P01648 mus musculu
33	337	30.1	111	1 KV3K_MOUSE	P01663 mus musculu

34	337	30.1	111	1 KV3L_MOUSE	P01664 mus musculu
35	336	30.0	111	1 KV3S_MOUSE	P01671 mus musculu
36	335	29.9	108	1 KV1H_HUMAN	P01600 homo sapien
37	335	29.9	108	1 KV1N_HUMAN	P01606 homo sapien
38	335	29.9	108	1 KV5J_MOUSE	P01643 mus musculu
39	333.5	29.8	109	1 KV3G_HUMAN	P04206 homo sapien
40	332	29.6	108	1 KV1B_HUMAN	P01594 homo sapien
41	332	29.6	108	1 KV1S_HUMAN	P01611 homo sapien
42	331.5	29.6	110	1 KV3P_MOUSE	P01668 mus musculu
43	331	29.5	108	1 KV5K_MOUSE	P01644 mus musculu
44	330	29.4	111	1 KV3M_MOUSE	P01665 mus musculu
45	330	29.4	111	1 KV3O_MOUSE	P01667 mus musculu

## ALIGNMENTS

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RESULT 1
KAC_MOUSE STANDARD: PRT: 106 AA.
ID KAC_MOUSE
AC P01837;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN C REGION.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE (MOPC 21).
RX MEDLINE=73053310; PubMed=4638343;
RA Svastl J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
RN [2]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svastl J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
RN [3]
RP SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
RX MEDLINE=79084137; PubMed=103625;
RA Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
RT "Complete sequence of constant and 3' noncoding regions of an
immunoglobulin mRNA using the dideoxynucleotide method of RNA
sequencing.";
RL Cell 15:1067-1075(1978).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=81191915; PubMed=6262318;
RA Max E.E., Maizel J.V. Jr., Leder P.;
RT "The nucleotide sequence of a 5.5-kilobase DNA segment containing the
mouse kappa immunoglobulin J and C region genes.";
RL J. Biol. Chem. 256:5116-5120(1981).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198949; PubMed=6785724;
RA Altenburger W., Neumayer P.S., Steilmetz M., Zachau H.G.;
RT "DNA sequence of the constant gene region of the mouse immunoglobulin
kappa chain.";
RL Nucleic Acids Res. 9:971-981(1981).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=88329081; PubMed=3138116;
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RA de Waele P., Feys V., van de Voerde A., Molemans F., Fiers W.;  
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin  
RT directed against the tumour marker human placental alkaline  
RT phosphatase";  
RL Eur. J. Biochem. 176:287-295(1988).  
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CC -----  
CC EMBL: V00807; CAA24189.1; -  
DR PIR: A02119; KIMS.  
DR PIR: S01320; S01320.  
DR InterPro: IPR000495; -  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; 1g; 1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 106 106  
SQ SEQUENCE 106 AA; 11778 MW; 4B51F5EFA9BAEB5 CRC64;  
  
Query Match 50.1%; Score 562; DB 1; Length 106;  
Best Local Similarity 99.1%; Pred. No. 1e-37;  
Matches 105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 109 ADAAPTYSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 168  
DB 1 ADAAPTYSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 60  
QY 169 KDSYMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 214  
DB 61 KDSYMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 106  
  
RESULT 2  
KACA\_RAT STANDARD; PRT; 106 AA.  
AC P01836;  
DT 21-JUL-1986 (rel. 01, Created)  
DT 21-JUL-1986 (rel. 01, Last sequence update)  
DT 15-JUL-1999 (rel. 38, Last annotation update)  
DE IG KAPPA CHAIN C REGION, A ALLELE.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DA;  
RX MEDLINE=82082587; PubMed=6273908;  
RA Sheppard H.W., Gutman G.A.;  
RT "Allelic forms of rat kappa chain genes: evidence for strong  
RT selection at the level of nucleotide sequence";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).  
DR InterPro: IPR000495; -  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; 1g; 1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DISULFID 26 86  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
SQ SEQUENCE 106 AA; 11732 MW; B7E120D9700DD66 CRC64;

Query Match 43.2%; Score 484; DB 1; Length 106;  
Best Local Similarity 84.9%; Pred. No. 1.3e-31;  
Matches 90; Conservative 10; Mismatches 6; Indels 0; Gaps 0;  
  
QY 109 ADAAPTYSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 168  
DB 1 ADAAPTYSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 60  
QY 169 KDSYMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 214  
DB 61 KDSYMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 106  
  
RESULT 3  
KACA\_RAT STANDARD; PRT; 106 AA.  
AC P01835;  
DT 21-JUL-1986 (rel. 01, Created)  
DT 21-JUL-1986 (rel. 01, Last sequence update)  
DT 15-JUL-1999 (rel. 38, Last annotation update)  
DE IG KAPPA CHAIN C REGION, B ALLELE.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LOU;  
RX MEDLINE=82082587; PubMed=6273908;  
RA Sheppard H.W., Gutman G.A.;  
RT "Allelic forms of rat kappa chain genes: evidence for strong  
RT selection at the level of nucleotide sequence";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).  
RN [2]  
RP SEQUENCE (BENCE-JONES PROTEIN S211).  
RX MEDLINE=75212238; PubMed=807630;  
RA Starace V., Querinjean P.;  
RT "The primary structure of a rat kappa Bence Jones protein:  
RT phylogenetic relationships of V- and C-region genes";  
RL J. Immunol. 115:59-62(1975).  
DR PIR: A02117; K1RTB.  
DR InterPro: IPR000495; -  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; 1g; 1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DISULFID 26 86  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
FT CONFLICT 2 2 D -> N (IN REF. 2).  
FT CONFLICT 30 30 N -> K (IN REF. 2).  
FT CONFLICT 48 48 MISSING (IN REF. 2).  
FT CONFLICT 79 79 E -> Q (IN REF. 2).  
FT CONFLICT 87 87 E -> Q (IN REF. 2).  
FT CONFLICT 98 98 V -> VV (IN REF. 2).  
FT CONFLICT 100 100 S -> N (IN REF. 2).  
SQ SEQUENCE 106 AA; 11601 MW; 4CFA7CA820D1CA36 CRC64;  
  
Query Match 41.8%; Score 469; DB 1; Length 106;  
Best Local Similarity 81.1%; Pred. No. 1.9e-30;  
Matches 86; Conservative 12; Mismatches 8; Indels 0; Gaps 0;  
  
QY 109 ADAAPTYSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 168  
DB 1 ADAAPTYSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 60  
QY 169 KDSYMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 214  
DB 61 KDSYMSSTLTITKADYSHNLTYCEVYHKTSSSPYKSFNNEC 106  
  
RESULT 4

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP  
RQ MEDLINE=83271467; PubMed=6877353;  
RA Käräinen M., Griffiths G.M., Markham A.F., Milstein C.;  
RT "mRNA sequences define an unusually restricted IgC response to 2-phenylloxazolone and its early diversification.";  
RL Nature 304:320-324(1983).  
CC -I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.  
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CC DR EMBL; K00735; AAA38680.1; -.  
DR InterPro; IPR003006; -.  
DR Pfam; PF00047; 1g; 1.  
KM Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 23 FRAMENOR 1.  
FT 24 33 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 34 48 FRAMEWORK 2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 56 87 FRAMEWORK 3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 97 106 FRAMEWORK 4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON_TER 107 107  
SQ SEQUENCE 107 AA; 11561 MW; 6f94284ecfa68E6 CRC64;  
  
Query Match 38.4%; Score 430.5; DB 1; Length 107;  
Best Local Similarity 80.4%; Pred.No. 2e-27;  
Matches 86; Conservative 8; Mismatches 10; Indels 3; Gaps 2;  
  
Dy 3 VLTPSPALMSAPCKVKMTKCRASSVSSYTLHWVRKSGASPKLIYSTSLAGVPAR 62  
| | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | |  
Db 3 VLTPSPALMSASPCKKYTMTCSSASSV--STWHWYQQSGTSPPKWIYDTSKLAGVPAR 60  
  
Qy 63 FSSGSGSSTSGLTTISVAEDAAATYYCOOYSGY-NTEFGSKTKLEKR 108  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 61 FSSGGSATSLSLTITSMQAEDAATFYCGOWSNPLTFPAGIKRLLEKR 107  
  
RESULT 6  
KV6I.MOUSE STANDARD; PRT; 107 AA.  
AC ID KV6I.MOUSE P04943;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-VI REGION NOG-8.3.1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP  
RQ SEQUENCE FROM N.A.  
RX MEDLINE=83271467; PubMed=6877353;  
RA Käräinen M., Griffiths G.M., Markham A.F., Milstein C.;  
RT "mRNA sequences define an unusually restricted IgC response to 2-phenylloxazolone and its early diversification.";  
RL Nature 304:320-324(1983).  
CC -I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.  
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DR EMBL: K00740; AAA38685.1; -  
DR InterPro: IPR003006; -  
KW Pfam: PF00047; 1g; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 23  
FT DOMAIN 24 33  
FT DOMAIN 34 48  
FT DOMAIN 49 55  
FT DOMAIN 56 87  
FT DOMAIN 88 96  
FT DOMAIN 97 106  
FT DISULFID 23 87  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11572 MW; 6f694824ECF0C8E6 CRC64;

Query Match  
Best Local Similarity 38.0%; Score 425.5; DB 1; Length 107;  
Matches 85; Conservative 8; Mismatches 11; Indels 3; Gaps 2;

OY 3 VLTQSPALMSASPGKVTMTCSRASSVSSSYLHWYRQKSGASPKLMTYSTNLASGVPAR 62  
DB 3 VLTQSPALMSASPGKVTMTCSRASSV--SYMHYQOKSGTSPKRWIYDTSKLASGVPAR 60  
OY 63 FSGSGGTSTSLTSSVEAEADATYYCOQYSGY-RTFGGGTKLEIKR 108  
DB 61 FSGSGGTSTSLTSSVEAEADATYYCOQMSNPFLTFGAGTKLEIKR 107

## RESULT 7

KV6G\_MOUSE  
ID KV6G\_MOUSE STANDARD; PRT; 107 AA.

AC P04942;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-VI REGION NQ5-61.1.2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=83271467; PubMed=6877353;  
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "mRNA sequences define an unusually restricted IgG response to 2-  
phenylloxazolone and its early diversification".  
RL Nature 304:320-324(1983).

CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

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CC EMBL: K00739; AAA38684.1; -  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; 1g; 1.

KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 23  
FT DOMAIN 24 33  
FT DOMAIN 34 48  
FT DOMAIN 49 55  
FT DOMAIN 56 87  
FT DOMAIN 88 96

CC COMPLEMENTARITY-DETERMINING 1.  
CC COMPLEMENTARITY-DETERMINING 2.  
CC COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 97 106  
FT DISULFID 23 87  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11605 MW; CAC64284EFC8550 CRC64;

Query Match  
Best Local Similarity 37.9%; Score 424.5; DB 1; Length 107;  
Matches 85; Conservative 8; Mismatches 11; Indels 3; Gaps 2;

OY 3 VLTQSPALMSASPGKVTMTCSRASSVSSSYLHWYRQKSGASPKLMTYSTNLASGVPAR 62  
DB 3 VLTQSPALMSASPGKVTMTCSRASSV--SYMHYQOKSGTSPKRWIYDTSKLASGVPAR 60  
OY 63 FSGSGGTSTSLTSSVEAEADATYYCOQYSGY-RTFGGGTKLEIKR 108  
DB 61 FSGSGGTSTSLTSSVEAEADATYYCOQMSNPFLTFGAGTKLEIKR 107

## RESULT 8

KV6G\_MOUSE  
ID KV6G\_MOUSE STANDARD; PRT; 107 AA.

AC P04941;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-VI REGION NQ2-48.2.2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=83271467; PubMed=6877353;  
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "mRNA sequences define an unusually restricted IgG response to 2-  
phenylloxazolone and its early diversification".  
RL Nature 304:320-324(1983).

CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

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CC EMBL: K00737; AAA38682.1; -  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; 1g; 1.

KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 23  
FT DOMAIN 24 33  
FT DOMAIN 34 48  
FT DOMAIN 49 55  
FT DOMAIN 56 87  
FT DOMAIN 88 96  
FT DOMAIN 97 106  
FT DISULFID 23 87  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11556 MW; 7248DA9EF354934 CRC64;

Query Match  
Best Local Similarity 37.6%; Score 421.5; DB 1; Length 107;  
Matches 84; Conservative 9; Mismatches 11; Indels 3; Gaps 2;

OY 3 VLTQSPALMSASPGKVTMTCSRASSVSSSYLHWYRQKSGASPKLMTYSTNLASGVPAR 62  
DB 3 VLTQSPALMSASPGKVTMTCSRASSV--SYMHYQOKSGTSPKRWIYDTSKLASGVPAR 60  
OY 63 FSGSGGTSTSLTSSVEAEADATYYCOQYSGY-RTFGGGTKLEIKR 108

OX	NCHI_TaxID=10090;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=79082830; PubMed=103573;
RA	Rao D.N., Rudnikoff S., Potter M.;
RT	"Kappa Chain variable regions from three galactan binding myeloma proteins ";
RL	Biochemistry 17:5555-5559(1978).
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
DR	PIR: A01941; KVMXX4.
DR	HSSP: P01679; 2FBJ.
DR	InterPro: IPR003006; -.
KW	Pfam; Pf00047; 1g; 1.
FT	Immunoglobulin V region.
FT	DOMAIN 1 23 FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 2 34 48 FRAMEWORK 2. FRAMEWORK 2.
FT	DOMAIN 3 49 55 COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3.
FT	DOMAIN 4 56 87 FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3. FRAMEWORK 4.
FT	DOMAIN 5 88 96 COMPLEMENTARITY-DETERMINING 4. FRAMEWORK 4. BY SIMILARITY.
FT	DISULFD 97 106
FT	NON_TER 107 107
SO	SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;
Query Match	
Best Local Similarity	36.7%; Score 411.5; DB 1; Length 107;
Matches	85; Conservative 78.0%; Pred. No. 6.1e-26; Mismatches 13; Indels 3; Gaps 2;
OY	1 ENVTQSPALMSASGEKVMTGRASSVSSSYLHWYOKSGASKMLTYSTSNLASGP 60           : : : : :           : : : : :           : : : : :           DB
OY	1 EIVLTQSPAITAAASIGKVVTTICSASSV--SYMHWYOKSGTSKPWIYEISKLASGV 58           : : : : :           : : : : :           : : : : :           OY
OY	61 ARFGSSGGSSTSLTSSIVEADATFYTCQQQS-CYRFEGGKTLEIKR 108           : : : : :           : : : : :           : : : : :           DB
OY	59 ARFGSSGGSSTSLTSSIMEADAIIYCQOWNPYLMTFGGGTKEIKR 107           : : : : :           : : : : :           : : : : :           RESULT 11
KVD_MOUSE	STANDARD; PRT; 107 AA.
ID	KVD_MOUSE STANDARD; PRT; 107 AA.
AC	P01678;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG KAPPA CHAIN V-VI REGION SAPC 10.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCHI_TaxID=10090;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=81054757; PubMed=6776525;
RA	Rudnikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT	"Kappa Chain joining segments and structural diversity of antibody combining sites ";
RL	Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
DR	PIR: A01941; KVMXX4.
DR	HSSP: P01679; 2FBJ.
DR	InterPro: IPR003006; -.
KW	Pfam; PF00047; 1g; 1.
FT	Immunoglobulin V region.
FT	DOMAIN 1 23 FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 2 34 48 FRAMEWORK 2. FRAMEWORK 2.
FT	DOMAIN 3 49 55 COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3.
FT	DOMAIN 4 56 87 FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3. FRAMEWORK 4.
FT	DOMAIN 5 88 96 COMPLEMENTARITY-DETERMINING 4. FRAMEWORK 4. FRAMEWORK 4.
FT	DOMAIN 6 97 106 COMPLEMENTARITY-DETERMINING 5. FRAMEWORK 5.

FT DISULFID 23 87 BY SIMILARITY.  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA: 11554 MW: 27A2D022A5EC34D7 CRC64;

Query Match 36.7%; Score 411.5; DB 1; Length 107;  
 Best Local Similarity 78.0%; Pred. No. 6.1e-26;  
 Matches 85; Conservative 8; Mismatches 13; Indels 3; Gaps 2;

OY 1 ENVTQSPAIMSAPGEKVTMTCRASSVSSSYLHWYRKGSGAPKLMYTSNLSAGVP 60  
 1 EIVLTQSPAIMSAPGEKVTMTCRASSVSSSYLHWYRKGSGAPKLMYTSNLSAGVP 58

OY 61 ARPSGSGSTSYSLTSSVEADATYTCQOYS-GYRFGGSGTKLEIKR 108  
 59 ARPSGSGSTSYSLTSSVEADATYTCQOYNNYPLTFGGSGTKLEIKR 107

RESULT 12

KV6C\_MOUSE STANDARD; PRT; 108 AA.

AC P04945;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-VI REGION NQ2-6.1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=83271467; PubMed=6877353;

RA Kaathinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "mRNA sequences define an unusually restricted IgG response to 2-

RT phenylloxazalone and its early diversification".

RL Nature 304:320-324(1983).

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 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: K00746; AAA38691.1; -

DR InterPro: IPR003006; -

DR Pfam: PF00047; Ig; 1.

KM Immunoglobulin V region; Hybridoma.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 2 34 48 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 3 49 55 FRAMEWORK 2.

FT DOMAIN 4 56 87 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 5 88 98 FRAMEWORK 3.

FT DOMAIN 6 99 108 COMPLEMENTARITY-DETERMINING 3.

FT DISULFID 23 87 BY SIMILARITY.

FT NON\_TER 108 108

SQ SEQUENCE 108 AA: 11713 MW: DABF235CD9680AC6 CRC64;

Query Match 36.4%; Score 407.5; DB 1; Length 108;  
 Best Local Similarity 75.0%; Pred. No. 1.3e-25;  
 Matches 81; Conservative 12; Mismatches 10; Indels 5; Gaps 2;

OY 3 VITQSPAIMSAPGEKVTMTCRASSVSSSYLHWYRKGSGAPKLMYTSNLSAGVP 62  
 3 LITQSPAIMSAPGEKVTMTCRASSVSSSYLHWYRKGSGAPKLMYTSNLSAGVP 60

OY 63 FSGSGSTSYSLTSSVEADATYTCQOYSG---RTFGGSGTKLEIKR 107  
 61 FSGSGSTSYSLTSSVEADATYTCQOYSYPPMLTFGGSGTKLEIKR 108

RESULT 13  
 KV6C\_MOUSE STANDARD; PRT; 107 AA.

AC P01676;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-VI REGION XRPC 24.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE.

RA Rao D.N., Rudikoff S., Potter M.;

RT "k Chain variable regions from three galactan binding myeloma

RT proteins".

RL Biochemistry 17:555-5559(1978).

CC -I MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT

CC BIND GALACTAN

DR PIR: A01941; KVMX4.

DR HSSP: P01679; 2F8J.

DR InterPro: IPR003006; -

DR Pfam: PF00047; Ig; 1.

KM Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 2 34 48 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 3 49 55 FRAMEWORK 2.

FT DOMAIN 4 56 87 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 5 88 96 FRAMEWORK 3.

FT DOMAIN 6 97 106 COMPLEMENTARITY-DETERMINING 3.

FT DISULFID 23 87 BY SIMILARITY.

FT NON\_TER 107 107

SQ SEQUENCE 107 AA: 11584 MW: 36E6D022A5EC34D7 CRC64;

Query Match 36.2%; Score 405.5; DB 1; Length 107;  
 Best Local Similarity 77.1%; Pred. No. 1.8e-25;  
 Matches 84; Conservative 8; Mismatches 14; Indels 3; Gaps 2;

OY 1 ENVTQSPAIMSAPGEKVTMTCRASSVSSSYLHWYRKGSGAPKLMYTSNLSAGVP 60  
 1 EIVLTQSPAIMSAPGEKVTMTCRASSVSSSYLHWYRKGSGAPKLMYTSNLSAGVP 58

OY 61 ARPSGSGSTSYSLTSSVEADATYTCQOYS-GYRFGGSGTKLEIKR 108  
 59 ARPSGSGSTSYSLTSSVEADATYTCQOYNNYPLTFGGSGTKLEIKR 107

RESULT 14

ID KV6C\_MOUSE STANDARD; PRT; 107 AA.

AC P01677;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-VI REGION TEPC 60L/TEPC 19L.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE (TEPC 60L).

RA MEDLINE=79082830; PubMed=103573;

RA Rao D.N., Rudikoff S., Potter M.;

RT "k Chain variable regions from three galactan binding myeloma

RT proteins".

RL Biochemistry 17:555-5559(1978).

RL [2]



